

08/06/47

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using SW model

Run on: April 23, 2003, 07:28:09 ; Search time 50 Seconds  
(without alignments)  
1543.919 Million cell updates/sec

Title: US-10-034-849-2

Perfect score: 4168  
Sequence: 1 MTEVVFVLDSSYEVEVKEP.....LKASATGQKTLFDLAKSK 803

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3033.5	72.4	803	2 B56277	DNA-directed DNA p
2	2434	58.1	784	2 E72515	probable DNA-direc
3	2266	53.6	781	2 UC7382	DNA-directed DNA p
4	1581	37.8	781	2 A69312	DNA polymerase B1
5	1287	30.7	764	2 S75407	probable DNA-direc
6	1236.5	29.5	775	2 S35543	DNA-directed DNA p
7	1207.5	28.8	771	2 C75023	DNA polymerase I p
8	1197.5	28.6	775	2 S67920	DNA-directed DNA p
9	965.5	23.1	1312	2 S68593	DNA-directed DNA p
10	955.5	22.8	1235	2 C71210	probable DNA-direc
11	915	21.8	586	2 C69028	DNA-dependent DNA
12	771.5	18.4	1086	2 T40242	DNA-directed DNA p
13	768.5	18.4	1670	2 S71551	DNA-directed DNA p
14	763.5	18.2	1086	2 T43266	DNA-directed DNA p
15	760.5	18.2	1107	1 A41618	DNA-directed DNA p
16	757.5	18.1	1106	1 A39299	DNA-directed DNA p
17	751	17.9	1038	1 UC5757	DNA-directed DNA p
18	749	17.9	1038	2 T18222	DNA polymerase del
19	743.5	17.8	1105	1 S40243	DNA-directed DNA p
20	741.5	17.7	1088	2 T05731	DNA-directed DNA p
21	731.5	17.5	1084	1 S19661	DNA-directed DNA p
22	718.5	17.2	901	2 B84210	DNA polymerase B1
23	713	17.0	1702	2 S42459	DNA-directed DNA p
24	705	16.8	1094	2 S22573	DNA-directed DNA p
25	691.5	16.5	1097	1 RNBYL3	DNA-directed DNA p
26	671	16.0	1634	2 B64410	DNA-directed DNA p
27	649.5	15.5	879	2 A56277	DNA-directed DNA p
28	647.5	15.5	872	2 UC7380	DNA-directed DNA p
29	628.5	15.0	875	2 UC5186	DNA-directed DNA p

30	625.5	14.9	959	2 F72763	probable DNA-direc
31	598.5	14.3	882	2 S23019	DNA-directed DNA p
32	598	14.3	1081	2 T20658	hypothetical prote
33	594.5	14.2	882	2 F90201	DNA polymerase I (
34	579.5	13.8	1462	1 DJH0AC	DNA-directed DNA p
35	578	13.8	1465	2 S45628	DNA-directed DNA p
36	569	13.6	787	2 E82237	DNA polymerase II
37	564.5	13.5	844	2 T31321	DNA-directed DNA p
38	527.5	12.6	787	2 G83410	DNA polymerase II
39	526	12.6	3122	2 T17202	DNA-directed DNA p
40	524.5	12.5	1015	1 DJBE2L	DNA-directed DNA p
41	523.5	12.5	1339	1 S20052	DNA-directed DNA p
42	517	12.3	1505	2 S28079	DNA-directed DNA p
43	515	12.3	1009	1 DJBEM2	DNA-directed DNA p
44	511	12.2	1026	2 T03108	DNA-directed DNA p
45	508.5	12.1	1513	2 T28158	probable DNA-direc

## ALIGNMENTS

### RESULT 1

B56277  
DNA-directed DNA polymerase (EC 2.7.7.7) II - Pyrodicticum occultum

C/Species: Pyrodicticum occultum  
C/Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 20-Jun-2000

C/Accession: B56277  
R/Uemori, T.; Ichino, Y.; Doi, H.; Kato, I.

J. Bacteriol. 177, 2164-2177, 1995

A/Title: The hyperthermophilic archaeon Pyrodicticum occultum has two alpha-like DNA po

A/Reference number: A56277; MUID:95238290; PMID:7721707

A/Accession: B56277

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-803 <UEM>

A/Cross-references: GB:D38574; NID:9807829; PIDN:BA07580.1; PID:9807830

C/Superfamily: herpesvirus DNA-directed DNA polymerase

C/Keywords: nucleotidyltransferase

Query Match	72.4%	Score 3033.5	DB 2	Length 803
Best Local Similarity	70.9%	Pred. No. 1.4e-176		
Matches 571	Conservative 106	Mismatches 121	Indels 7	Gaps 5
QY	1	MTEVVFVLDSSYEVEVKEP	1	1
DB	1	MTETIEFVLDSSYEVEVKEP	1	1
QY	58	VAKRIPALSPSPITIGVEDDGRKYFGRRRLRTVLPEAVREYRELKRVNVDGEDVL	117	
DB	61	IAASIRRLSVSPPIIDAKPLDKRFFGRPKAVKTTMTLPESVRRHREAVKKBGVDSL	120	
QY	118	BADIRPAMVYLDHDLFPTWYRVEAEPLNKGFRVDKRVYVKSRRPDLGALAPTKL	177	
DB	121	EDIRPAMVYLDKRLYPTVTRIPEDAGRNPRGRVDRVYVAGDPEL--ADIRIDL	178	
QY	178	PDLRIAPDIEVYSKQSGSPRPERDPIYAVXTDGDDEVFLAEGKDKPREFVEYK	237	
DB	179	PMRLVAPDIEVYSRSGSPNPARDPYIYSLDSSEKELIAEGHDDRRVLRFEVEYK	238	
QY	238	RDPDPIVGYNNHHPWVYLLARARLIGKLVTRVGAEPSTSVGHVSGRLAVDLY	297	
DB	239	ADPDPIVGYNNHHPWVYLLARARLIGKLVTRVGAEPSTSVGHVSGRLAVDLY	298	
QY	298	DVAEEMPEIKISLEVAEYLVGMKSKSEVYINMWEIPYMPDPKKRPILLQYARDVNA	357	
DB	299	DVAEEMPEIKMKTLSEVAEYLVGMKSKSEVYINMWEIPYMPDDEKKRQLERYALDDVNA	358	
QY	358	TGGLAEKILPFAIQLSYVTGLPLDVGAMSVGRLEWYLIRAPFKKELVPRVERPEET	417	
DB	359	TGGLAEKMLPFAIQLSYVTGLPLDVGAMSVGRLEWYLIRAPFKKELVPRVERPEET	418	
QY	418	YKGLVLEPLRGVHERIAVLDFSSMTYPMIMKYNQPDVLPVPGKCGSC--CQWEPEYK	476	
DB				

Db 419 YKAAVTLKPLKGVHENVVLDSSMTYPSIMIKYVGPDTIVDDPSECRKYGCCYVAPEVG 478  
 Qy 477 HRPFRCPGFEKTVLERLELRKVRBAEMKKCPDPSPEYRLDEROKALKYLANASYGM 536  
 Db 479 HRPFRSPGFEKTVLERLELRKVRBAEMKKCPDPSPEYRLDEROKALKYLANASYGM 538  
 Qy 537 GWSGARWYCRECAAVTAMGSHLIRTAINTAKLGLKVIYGDTSLSFYDPEKVENFIK 596  
 Db 539 GWSHARWYCKCAEAVTAMGSHLIRTAINTAKLGLKVIYGDTSLSFYDPEKVENFIK 598  
 Qy 597 IIRKELGEITLKVYKRLFTTEBAKRYAGLLEGRIDIVGEAVRGWMCCLAKVQKV 656  
 Db 599 FVEKELGEITLKVYKRLFTTEBAKRYAGLLEGRIDIVGEAVRGWMCCLAKVQKV 658  
 Qy 657 VEIYLTSEVNAKAVYKRYKVELEBKVPLEKTYIMKTLSSRLSEYTBAPHVAAARM 716  
 Db 659 AEIYLTGNVNDKALSYIREVVKOLREGKVPITKLIIMKTLSSRLSEYTBAPHVAAARM 718  
 Qy 717 LSAGRVSPGDKIGYIVYKGGRIISQAMPYFMVDPSPQIDVTYVYDHOIIPALIRILGY 776  
 Db 719 KEAGREVSPGDKIGYIVYKGGRIISQAMPYFMVDPSPQIDVTYVYDHOIIPALIRILGY 778  
 Qy 777 FGITEKKLKASATQKTLFDFLAKK 801  
 Db 778 FGITEKKLKASATQKTLFDFLAKK 802

## RESULT 2

B72515  
 probable DNA-directed DNA polymerase APE2098 - Aeropyrum pernix (strain KI)  
 C/Species: Aeropyrum pernix  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
 C/Accession: B72515  
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999  
 A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum A/Reference number: A72450; MUID:99310339; PMID:10382966  
 A/Accession: B72515  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-784 <KAW>  
 A/Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BA01109.1; PID:95105797  
 A/Experimental source: strain KI  
 C/Genetics:  
 A/Gene: APE2098  
 C/Superfamily: herpesvirus DNA-directed DNA polymerase

Query Match 58.1%; Score 2434; DB 2; Length 784;  
 Best local similarity 59.1%; Pred. No. 3.7e-140;  
 Matches 469; Conservative 113; Mismatches 189; Indels 22; Gaps 5;

Qy 17 GKEPVIIWGIAENGERVLLIDRSFRPYFYALLAPGADPKQVAKIRALSRKSPITIGVE 76  
 Db 3 GSTPVIILMGAGDSRVVVFYGEFRPYFYVLDGSGVGLDQLAAMIRLRSPSSDILSEV 62  
 Qy 77 DDKRYFPRPRVLRITVLPAAVREYRELTVNGVDEVLEADIRFAMRYLIDHDLPPP 136  
 Db 63 RVRRRFIRGEVBALKVTLIVPASVREYREAVRRLGVRVDEADIRFALRPIDNLTVM 122  
 Qy 137 TWYREABFLNKGFRVVKYLV-----KSRPPLVGEALAPTKLPDLRIALFDI 187  
 Db 123 RMYVAEVEVAVPHGYSVDRAYTLISGDIRBDETRIQEDPLKQ-----LRVARDI 172  
 Qy 188 EYVSKQSPREPRDPVIVIAVKTDDGDEVLPFAEGKDRKPIREVEYVVKYDPDIIVGY 247  
 Db 173 EYVSKMRPDPKDPVIMIGIQAGGELEIEAEDRSKVKYAGVREYKSLDPPVIVGY 232  
 Qy 248 NNNHFDMPYLLRRARILGIDVTRVGAPEPTTVHGVAVYGRANVLVDYAEEMPEIK 307  
 Db 173 NNNHFDMPYLLRRARILGIDVTRVGAPEPTTVHGVAVYGRANVLVDYAEEMPEIK 291  
 A:EYGVKKSERVIINMEIPDWDPPKRRLLQYARDVATYGLAKILP 367

Db 292 VKTLEEVADYLGAVKIGERTLETMOIGEWYDPSKREILRKLRDVRSTMLAEKFLP 351  
 Qy 368 FALQSLVYVGLPLDOYGAMSVGFRLEMYVLIIRAFKOKELVNVNREPEEYRGAVILEPL 427  
 Db 352 FGABLSQVSLPLDOYMAASVGFRLERLIRAKAGELVFNKVERSEGYAGAILVRPK 411  
 Qy 428 RGVHENIAVDFSSMYPNIMIKYVGPDTIVRPGKCGECGCEWABEVKRFRCPPGF 487  
 Db 412 PGVHEDIAVDFASMYPNIMIKYVGPDTIVRPGEEYGESEVYTADEVGHKFRKSPGF 471  
 Qy 488 KTVLERLELRKVRBAEMKKYPPDPSPEYRLDEROKALKYLANASYGMGSGARWYCRE 547  
 Db 472 KXILERFLSWRQIRSEMKGPPDPSPEYRLDEROKALKYLANASYGMGMPHARWYCRE 531  
 Qy 548 CAAVYAMGSHLIRTAINTAKLGLKVIYGDTSLSFYDPEKVENFIKIRKELGEIK 607  
 Db 532 CAEVYAMGSHLIRTAINTAKLGLKVIYGDTSLSFYDPEKVENFIKIRKELGEIK 591  
 Qy 608 LERVKRLFTTEBAKRYAGLLEGRIDIVGEAVRGWMCCLAKVQKVEIYLTSEVN 667  
 Db 592 VDKYRRVFTTEBAKRYAGLLEGRIDIVGEAVRGWMCCLAKVQKVEIYLTSEVN 651  
 Qy 668 KAVRYAKYKVELEBKVPLEKTYIMKTLSSRLSEYTBAPHVAAARMKLSAGRVSPG 727  
 Db 652 EAVDYANIEKLRQGVDRKLVIMKTLTRPSPMEARQPHYALALMERAGIKVEPGA 711  
 Qy 728 KIGYIVYKGGRIISQAMPYFMVDPSPQIDVTYVYDHOIIPALIRILGYFTEKKLKAS 787  
 Db 712 KIGYIVYKGGRIISQAMPYFMVDPSPQIDVTYVYDHOIIPALIRILGYFTEKKLKAS 770  
 Qy 788 ATGQKTLFDFLAKK 800  
 Db\* 771 GR-QSTLIDPMR 782

## RESULT 3

JC7382  
 DNA-directed DNA polymerase (BC 2.7.7.7) B3 - Sulfitisphaera ohwakensis  
 N/Alternate names: DNA polymerase alpha, beta, gamma; DNA polymerase I, II, III  
 C/Species: Sulfitisphaera ohwakensis  
 C/Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 31-Dec-2000  
 C/Accession: JC7382  
 R:Iwai, T.; Kurokawa, N.; Itoh, Y.H.; Kimura, N.; Horiuchi, T.  
 DNA Res. 7, 243-251, 2000  
 A/Title: Sequence analysis of three family B DNA polymerases from the thermocacidophil A/Reference number: JC7380  
 A/Accession: JC7382  
 A/Molecule type: DNA  
 A/Residues: 1-781 <IWA>  
 A/Cross-references: DDBJ:AB032376  
 C/Comment: This enzyme has both 3'-5' exonuclease and polymerase activities, and play C/Genetics:  
 A/Gene: B3  
 C/Keywords: DNA replication; exonuclease; metal binding; nucleotidyltransferase

Query Match 53.6%; Score 2246; DB 2; Length 781;  
 Best local similarity 54.3%; Pred. No. 9.9e-129;  
 Matches 432; Conservative 141; Mismatches 203; Indels 20; Gaps 10;

Qy 6 FTVLDSGYEVGKEPOVITWGIAENGERVLLIDRSFRPYFYALLAPGADPKQVAKIRAL 65  
 Db 5 FTLLDSGYDVVENKPYIYIWIIDEGNRVLLKSKFRPYFYALVDSYNDIRKEIKL 64  
 Qy 66 SRKSPPIGVEDDKKYPGRPRVLAIRTVLPAAVREYRELTVNGVDEVLEADIRFAM 125  
 Db 65 SKRSPPTSIDVEBKYPGSPVLAIRTVLPAAVREYRELTVNGVDEVLEADIRFAM 124  
 Qy 126 RYVLDHDLPEPTTVYVREABFLNKGFRVVKYLVVSRPPLVGEALAPTKLPDLRIALF 185  
 Db 125 RYVLDHDLPEPTTVYVREABFLNKGFRVVKYLVVSRPPLVGEALAPTKLPDLRIALF 177  
 Qy 186 DIEVSKQSPREPRDPVIVIAVKTDDGDEVLPFAEGKDRKPIREVEYVVKYDPDIIV 245

QY 421 ATVLEPLRGVHNIATVLDPSMYNIMIKYNGPDTLVPRGKCGCGGMBAPVYKRR 480  
 DB 421 ATVLEPLRGVHNIATVLDPSMYNIMIKYNGPDTLVPRGKCGCGGMBAPVYKRR 480  
 QY 481 RCPGPFKTVLELRLRLKRVRAEMKKYPPDSPERYLLDEROKALKVLNANASYGMGSG 540  
 DB 481 RCPGPFKTVLELRLRLKRVRAEMKKYPPDSPERYLLDEROKALKVLNANASYGMGSG 540  
 QY 541 AAWYCECAKAVTAMGRHLIRTAINTARKLGLKVIYGDTSLFVYDPEKVENFIKIKE 600  
 DB 541 AAWYCECAKAVTAMGRHLIRTAINTARKLGLKVIYGDTSLFVYDPEKVENFIKIKE 600  
 QY 601 ELGFEFKLEKTVNRLFFTEAKKRYAGLLEDRIDIVGFAVRGDMCELAECVTKVVEY 660  
 DB 601 ELGFEFKLEKTVNRLFFTEAKKRYAGLLEDRIDIVGFAVRGDMCELAECVTKVVEY 660  
 QY 661 LKTSVNVKAVEYRKIVKLEBEGKVPLEKLVIMKLSKLEETTEAPHVAAKRLMSAG 720  
 DB 661 LKTSVNVKAVEYRKIVKLEBEGKVPLEKLVIMKLSKLEETTEAPHVAAKRLMSAG 720  
 QY 721 YRVSPEDKIGYIVKGGGRISQRAPIFYVYKDPQSDIVTYVYDHOIIPALRLILGYFGIT 780  
 DB 721 YRVSPEDKIGYIVKGGGRISQRAPIFYVYKDPQSDIVTYVYDHOIIPALRLILGYFGIT 780  
 QY 781 EKKLKASATGOKTLFDFLAKSK 803  
 DB 781 EKKLKASATGOKTLFDFLAKSK 803

## RESULT 2

US-08-062-368-4  
 Sequence 4, Application US/08062368  
 Patent No. 5491086

## GENERAL INFORMATION:

APPLICANT: Gelfand, David H.  
 TITLE OF INVENTION: Purified Thermostable Nucleic Acid  
 TITLE OF INVENTION: Polymerases Enzyme From Pyrodicticum Species  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann-La Roche Inc.  
 STREET: 340 Kingsland Street  
 CITY: Nutley  
 STATE: New Jersey  
 COUNTRY: U.S.A.  
 ZIP: 07110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/062,368  
 FILING DATE: 19930514

## CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Stas Ph.D., Stacey R.  
 REGISTRATION NUMBER: 32,630  
 REFERENCE/DOCKET NUMBER: 8584

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 814-2863  
 TELEFAX: (510) 814-2977

## INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 803 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 062-368-4

72.3%, Score 3028.5, DB 1, Length 803;

Best Local Similarity 70.8%; Pred. No. 1e-270;  
 Matches 570; Conservative 106; Mismatches 122; Indels 7; Gaps 5;

QY 1 MTEVV-FTVLDSYVYVCKEPOVYIINGIAENGRVYLIDSFRYFALLAPGADP--KQ 57-  
 DB 1 MTEVIEFTLDSYVYVCKEPOVYIINGIAENGRVYLIDSFRYFALLAPGADP--KQ 57-  
 QY 58 VAQRIPLSRKSPILIGVEDKRYKGPAPRVLAIRTVLPAVAYEVELYKGVGVEDVL 117  
 DB 61 IAASTRILSVKSPILIAKPLDKRYFGAPRAVAKITMIPESVHYHRAVAKIKGVESL 120  
 QY 118 EADIFAPARVYLIDHLPFTYRVYAEAPLENKGPFRVDKVLVNSRPELVGEALAPTKL 177  
 DB 121 EADIFAPARVYLIDHLPFTYRVYAEAPLENKGPFRVDKVLVNSRPELVGEALAPTKL 178  
 QY 178 PDLRIAPDIYVSKSGSPRPERPVIVIAVTKDDGSEVLFIAGKDRKDIREFVEYVK 237  
 DB 179 PDMRLVAPDIYVSKSGSPRPERPVIVIAVTKDDGSEVLFIAGKDRKDIREFVEYVK 238  
 QY 238 RDPDIIYGVNNHFDWYLLRPARILGIDYTRRVAAEFTTSYHGVSVPGRLANDLY 297  
 DB 239 AADPDIIYGVNNHFDWYLLRPARILGIDYTRRVAAEFTTSYHGVSVPGRLANDLY 298  
 QY 298 DYAEEMPEIKIKSLSEVVAEYLGVMKSSRVIIINWEIPDYDDPKKRPILLQYADVDRA 357  
 DB 299 DYAEEMPEIKIKSLSEVVAEYLGVMKSSRVIIINWEIPDYDDPKKRPILLQYADVDRA 358  
 QY 358 TYGLAEKILPFAIQLSYVGLPLDQVGAMSVGFLEWTLIRAPFMKELVNNRVERPEET 417  
 DB 359 TYGLAEKILPFAIQLSYVGLPLDQVGAMSVGFLEWTLIRAPFMKELVNNRVERPEET 418  
 QY 418 YRGATVLEPLRGVHNIATVLDPSMYNIMIKYNGPDTLVPRGKCGCGGMBAPVYKRR 476  
 DB 419 YRGATVLEPLRGVHNIATVLDPSMYNIMIKYNGPDTLVPRGKCGCGGMBAPVYKRR 478  
 QY 477 HFRRCPPGPFKTVLELRLRLKRVRAEMKKYPPDSPERYLLDEROKALKVLNANASYGM 536  
 DB 479 HFRRCPPGPFKTVLELRLRLKRVRAEMKKYPPDSPERYLLDEROKALKVLNANASYGM 538  
 QY 537 GWSGARWYCRECAKAVTAMGRHLIRTAINTARKLGLKVIYGDTSLFVYDPEKVENFIK 596  
 DB 539 GWSGARWYCRECAKAVTAMGRHLIRTAINTARKLGLKVIYGDTSLFVYDPEKVENFIK 598  
 QY 597 IIKBELGPEIKLEKYKPLFTFEAKKRYAGLLEDRIDIVGFAVRGDMCELAECVTKV 656  
 DB 599 IIKBELGPEIKLEKYKPLFTFEAKKRYAGLLEDRIDIVGFAVRGDMCELAECVTKV 658  
 QY 657 VEIVLKTSEVNVKAVEYRKIVKLEBEGKVPLEKLVIMKLSKLEETTEAPHVAAKRL 716  
 DB 659 VEIVLKTSEVNVKAVEYRKIVKLEBEGKVPLEKLVIMKLSKLEETTEAPHVAAKRL 718  
 QY 717 LSAQYRVSPGDKIGYIVKGGGRISQRAPIFYVYKDPQSDIVTYVYDHOIIPALRLILGY 776  
 DB 719 LSAQYRVSPGDKIGYIVKGGGRISQRAPIFYVYKDPQSDIVTYVYDHOIIPALRLILGY 777  
 QY 777 FGIITEKKLKASATGOKTLFDFLAKSK 801  
 DB 778 FGIITEKKLKASATGOKTLFDFLAKSK 802

## RESULT 3

US-08-062-368-2  
 Sequence 2, Application US/08062368  
 Patent No. 5491086

## GENERAL INFORMATION:

APPLICANT: Gelfand, David H.  
 TITLE OF INVENTION: Purified Thermostable Nucleic Acid  
 TITLE OF INVENTION: Polymerases Enzyme From Pyrodicticum Species  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann-La Roche Inc.  
 STREET: 340 Kingsland Street